OM nucleic - nucleic search, using sw model

Run on: August 27, 2001, 18:00:22 ; Search time 193.18 Seconds
(without alignments)
2323.997 Million cell updates/sec

Title: US-09-784-340-3_COPY_197_911
Perfect score: 715
Sequence: 1 atgaggtctgacaagtcagc.....gttttatagtaaggcattag 715

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_0601:*
1: /SIDS1/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	470.6	65.8	515	20	AAV87412	EST clone BR77. H
	2	190.2	26.6	1976	21	AAZ95206	Human UDP-glucuron
	3	190.2	26.6	2312	21	AAZ95207	Human UGT2B15 exon
	4	186.8	26.1	1323	21	AAZ95193	Human UGT2B4 exon
	5	186.8	26.1	2092	21	AAZ95199	Human UDP-glucuron
	6	186.2	26.0	1650	21	AAC65396	Human carbohydrate
	7	179	25.0	2107	19	AAV15900	Uridine diphospho-
	8	172.4	24.1	1686	21	AAZ95201	Human UGT2B7 exon
	9	172.4	24.1	1854	21	AAZ95200	Human UDP-glucuron
	10	124	17.3	283	21	AAA87467	Rat hepatocyte car
c	11	81	11.3	936	22	AAF58252	Oligonucleotide D1
c	12	81	11.3	936	22	AAF58254	Oligonucleotide D1
c	13	81	11.3	936	22	AAF58257	Oligonucleotide D1
c	14	81	11.3	936	22	AAF58259	Oligonucleotide D2
c	15	81	11.3	936	22	AAF58262	Oligonucleotide D2
c	16	81	11.3	938	22	AAF58255	Oligonucleotide D1
	17	78.6	11.0	936	22	AAF58252	Oligonucleotide D1
	18	78.6	11.0	936	22	AAF58254	Oligonucleotide D1
	19	78.6	11.0	936	22	AAF58257	Oligonucleotide D1
	20	78.6	11.0	936	22	AAF58259	Oligonucleotide D2
	21	78.6	11.0	936	22	AAF58262	Oligonucleotide D2
	22	78.6	11.0	938	22	AAF58255	Oligonucleotide D1
	23	69.8	9.8	264	21	AAF15707	Human prostate can
	24	64.8	9.1	1048	13	AAQ33020	UGT1E Exon 1 from
	25	63.2	8.8	867	21	AAZ45113	UDP-glucuronosyltr
	26	55.2	7.7	867	21	AAZ45111	UDP-glucuronosyltr
	27	53.6	7.5	1105	13	AAQ33022	UGT1C Exon 1 from
	28	52.2	7.3	864	21	AAZ45110	UDP-glucuronosyltr
	29	52.2	7.3	2351	13	AAQ27369	HUG-Br1. Homo sap
	30	52	7.3	244	22	AAF58238	Oligonucleotide D1
	31	52	7.3	867	21	AAZ45112	UDP-glucuronosyltr
	32	49.2	6.9	861	21	AAZ45114	UDP-glucuronosyltr
	33	48.8	6.8	951	21	AAZ45115	UDP-glucuronosyltr
	34	48.8	6.8	1241	13	AAQ27368	UGT1F Exon 1 from
	35	48.8	6.8	2368	13	AAQ27370	HUG-Br2. Homo sap
	36	45.6	6.4	1120	13	AAQ33021	UGT1D Exon 1 from
c	37	43	6.0	244	22	AAF58238	Oligonucleotide D1
	38	42.4	5.9	759	21	AAZ45117	UDP-glucuronosyltr
	39	41.8	5.8	8318	20	AAX20264	Borrelia burgdorfe
	40	40.2	5.6	5194	20	AAX25885	C.albicans alpha-I
	41	40	5.6	1483	13	AAQ33023	UGT1BP Exon 1 from
c	42	38	5.3	163319	21	AAF22306	Arabidopsis thalia
	43	36.8	5.1	930	21	AAZ45116	UDP-glucuronosyltr
c	44	36.2	5.1	8011	19	AAV38336	Manic-depressive i
c	45	36.2	5.1	8065	19	AAV38335	Manic-depressive i

ALIGNMENTS

RESULT 1
AAV87412
ID AAV87412 standard; cDNA; 515 BP.
XX
AC AAV87412;
XX
DT 27-APR-1999 (first entry)
XX
DE EST clone BR77.
XX
KW Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX
OS Homo sapiens.
XX
PN WO9845435-A2.
XX
PD 15-OCT-1998.
XX
PF 10-APR-1998; 98WO-US06954.
XX
PR 10-APR-1997; 97US-0835913.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
PI Racie LA, Spaulding V, Treacy M;
XX
DR WPI; 1999-070076/06.
XX
PT New polynucleotides encoding human secreted proteins - derived from
PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,

PT ovary, pituitary, retina and colon cDNA libraries
XX
PS Claim 1; Page 556; 633pp; English.
XX
CC This sequence represents an expressed sequence tag (EST), and is a
CC polynucleotide of the invention. The polynucleotides of the invention are
CC all secreted EST sequences isolated from a variety of human tissue
CC sources. The EST sequences and proteins encoded by them are predicted to
CC have useful biological activities which would make them suitable for
CC treating, preventing or ameliorating medical conditions in humans and
CC animals, although no supporting data is given. Suggested activities
CC include nutritional activity, immune stimulating or suppressing activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity. The EST sequences are also stated to be useful for gene
CC therapy.
XX
SQ Sequence 515 BP; 148 A; 98 C; 122 G; 147 T; 0 other;

Query Match 65.8%; Score 470.6; DB 20; Length 515;
Best Local Similarity 99.2%; Pred. No. 4.9e-126;
Matches 473; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1 atgaggtctgacaagtcagctttggtatttctgctcctgcagctcttctgtgttggctgt 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      33 atgaggtctgacaagtcagctttggtatttctgctcctgcagctcttctgtgttggctgt 92

Qy      61 ggattctgtgggaaagtcctggtgtggccctgtgacatgagccattggcttaatgtcaag 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      93 ggattctgtgggaaagtcctggtgtggccctgtgacatgagccattggcttaatgtcaag 152

Qy     121 gtcattctagaagagctcatagtgagaggccatgaggtaacagtattgactcactcaaag 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     153 gtcattctagaagagctcatagtgagaggccatgaggtaacagtattgactcactcaaag 212

Qy     181 ccttcgttaattgactacaggaagccttctgcattgaaatttgaggtggtccatatgcca 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     213 ccttcgttaattgactacaggaagccttctgcattgaaatttgaggtggtccatatgcca 272

Qy     241 caggacagaacagaagaaaatgaaatatttgttgacctagctctgaatgtcttgccaggc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     273 caggacagaacagaagaaaatgaaatatttgttgacctagctctgaatgtcttgccaggc 332

Qy     301 ttatcaacctggcaatcagttataaaattaaatgatttttttgttgaaataagaggaact 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     333 ttatcaacctggcaatcagttataaaattaaatgatttttttgttgaaataagaggaact 392

Qy     361 ttaaaaatgatgtgtgagagctttatctacaatcagacacttatgaagaagctacaggaa 420
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     393 ttaaaaatgatgtgtgagagctttatctacaatcagacgcttatgaagaagctacaggaa 452

Qy     421 accaactacgatgtaacgcttatagaccctgtgattccccgtggagacctgatggct 477
          ||||||||||||||| |||||||||||||||||||||| |||||||||||| |||
Db     453 accaactacgatgtaatgcttatagaccctgtgattccctgtggagacctgatagct 509
```

RESULT 2
AAZ95206
ID AAZ95206 standard; DNA; 1976 BP.
XX
AC AAZ95206;
XX
DT 05-JUN-2000 (first entry)
XX
DE Human UDP-glucuronosyltransferase 2B15 nucleotide sequence.
XX
KW UDP-glucuronosyltransferase 2B15; UGT2B15; polymorphism; metabolism;
KW drug interaction; detect; human; single nucleotide polymorphism;
KW SNPs; ds.
XX
OS Homo sapiens.
XX
PN WO200006776-A1.
XX
PD 10-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US16675.
XX
PR 28-JUL-1998; 98US-0094391.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Galvin M, Miller A, Penny L, Riedy M;
XX
DR WPI; 2000-195321/17.
DR P-PSDB; AAY78935.
XX
PT Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT genotyping individuals to predict rate of metabolism of substrates and
PT for identifying potential drug interactions
XX
PS Disclosure; Page 56-59; 72pp; English.
XX
CC This sequence represents the human UDP-glucuronosyltransferase 2B15
CC (UGT2B15) gene. UDP-glucuronosyltransferase (UGTs) are a family of
CC enzymes that catalyse the glucuronic acid conjugation of a wide range of
CC endogenous and exogenous substrates. The UGT2B gene subfamily encode
CC steroid metabolizing isoforms in the liver. Alteration of the expression
CC or function of UGTs may effect drug metabolism. The invention relates to
CC non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC sequence polymorphisms (see AAZ95051-Z95110). Probes which detect the
CC UGT2B locus polymorphisms can be used to detect altered UGT2B metabolism
CC of a substrate in an individual. The nucleic acid molecules comprising a
CC human UGT2B sequence polymorphism can be used in screening assays for
CC genotyping individuals, also to predict their rate of metabolism of
CC UGT2B substrate, potential drug-drug interactions and adverse side
CC effects. The polymorphisms can be used as single nucleotide polymorphisms
CC (SNPs) for detecting genetic linkage related to phenotypic variation in
CC activity or expression of UGT2B protein. The polymorphism containing
CC nucleic acid molecules may also be used for generating genetically
CC modified non-human animals and for obtaining site specific gene
CC modification in cell lines.
XX
SQ Sequence 1976 BP; 594 A; 368 C; 419 G; 595 T; 0 other;

Query Match 26.6%; Score 190.2; DB 21; Length 1976;
Best Local Similarity 56.0%; Pred. No. 5.5e-45;
Matches 407; Conservative 0; Mismatches 308; Indels 12; Gaps 2;

```
Qy       1 atgaggtctgacaagtcagctttggtatttctgctcctgcagctcttctgt---gttggc 57
            | || ||||   || |   | |  || ||||||||  | ||||||   |||    || ||
Db       8 aggatgtctctgaaatggacgtcagtctttctgctgatacagctcagttgttacttttagc 67

Qy      58 tgtggattctgtgggaaagtcctggtgtggccctgtgacatgagccattggcttaatgtc 117
            | ||||  |||||| || || || |||||||||   ||    |||||||||| | ||| |
Db      68 tctggaagctgtggaaaggtgctagtgtggcccacagaatacagccattggataaatatg 127

Qy     118 aaggtcattctagaagagctcatagtgagaggccatgaggtaacagtattgactcactca 177
           |||   || || ||||||||  |   ||| || |||||||| || || |||||    ||
Db     128 aagacaatcctggaagagcttgttcagaggggtcatgaggtgactgtgttgacatcttcg 187

Qy     178 aagccttcgttaattgactacaggaagccttctgcattgaaatttgaggtggtccatatg 237
               || |  |  |  |   ||| ||  | |||||  | |||||  || ||    | ||
Db     188 gcttctactcttgtcaatgccagtaaatcatctgctattaaattagaagtttatcctaca 247

Qy     238 cc---------acaggacagaacagaagaaaatgaaata[illegible]tgttgacctagctctgaat 288
             |         | | ||      |||       |   | |||  | ||   |   |  ||
Db     248 tctttaactaaaaatgatttggaagattctcttctgaaaa[illegible]tctcgatagatggatatat 307

Qy     289 gtcttgccaggcttatcaacctggcaatcagttataaaattaaatgatttttttgttgaa 348
           |   |  ||       ||   |||  ||   ||  | ||||| | || || | |   |||
Db     308 ggtgtttcaaaaaatacattttggtcatatttttcacaattacaagaattgtgttgggaa 367
```

```
Qy    349 ataagaggaactttaaaaatgatgtgtgagagctttatctacaatcagacacttatgaag 408
Db    368 tattatgactacagtaacaagctctgtaaagatgcagttttgaataagaaacttatgatg 427

Qy    409 aagctacaggaaaccaactacgatgtaacgcttatagaccctgtgattccccgtggagac 468
Db    428 aaactacaagagtcaaagtttgatgtcattctggcagatgcccttaatccctgtggtgag 487

Qy    469 ctgatggctgagttgcttccagtccctttttgtgctcacacttagaacttctctaagaggc 528
Db    488 ctactggctgaactatttaacataccctttctgtacagtcttcgattctctgttggctac 547

Qy    529 aatatggagcgaagctgtgggaaacttccagctccactttcctatgtacctgtgcctatg 588
Db    548 acatttgagaagaatggtggaggatttctgttccctccttcctatgtacctgttgttatg 607

Qy    589 acaggactaacagacagaatgacctttctggaaagagtaaaaaattcaatgctttcagtt 648
Db    608 tcagaattaagtgatcaaatgattttcatggagaggataaaaaatatgatacatatgctt 667

Qy    649 ttgttccacttctggattcaggattacgactatcatttttgggaagagttttatagtaag 708
Db    668 tattttgacttttggtttcaaatttatgatctgaagaagtgggaccagttttatagtgaa 727

Qy    709 gcattag 715
Db    728 gttctag 734
```

RESULT 3
AAZ95207
ID AAZ95207 standard; DNA; 2312 BP.
XX
AC AAZ95207;
XX
DT 05-JUN-2000 (first entry)
XX
DE Human UGT2B15 exon 1 nucleotide sequence.
XX
KW UDP-glucuronosyltransferase 2B15; UGT2B15; polymorphism; metabolism;
KW drug interaction; detect; human; single nucleotide polymorphism;
KW SNPs; ds.
XX
OS Homo sapiens.
XX
PN WO200006776-A1.
XX
PD 10-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US16675.
XX
PR 28-JUL-1998; 98US-0094391.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Galvin M, Miller A, Penny L, Riedy M;
XX
DR WPI; 2000-195321/17.
XX
PT Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT genotyping individuals to predict rate of metabolism of substrates and
PT for identifying potential drug interactions -
XX
PS Example 3; Page 60-61; 72pp; English.
XX
CC This sequence represents the nucleotide sequence of exon 1 of the human
CC UDP-glucuronosyltransferase 2B15 (UGT2B15) gene.
CC UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse
CC the glucuronic acid conjugation of a wide range of endogenous and
CC exogenous substrates. The UGT2B gene subfamily encode steroid
CC metabolizing isoforms in the liver. Alteration of the expression or
CC function of UGTs may effect drug metabolism. The invention relates to
CC non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC can be used to detect altered UGT2B metabolism of a substrate in an
CC individual. The nucleic acid molecules comprising a human UGT2B sequence
CC polymorphism can be used in screening assays for genotyping individuals,
CC also to predict their rate of metabolism of UGT2B substrate, potential
CC drug-drug interactions and adverse side effects. The polymorphisms can be
CC used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC linkage related to phenotypic variation in activity or expression of
CC UGT2B protein. The polymorphism containing nucleic acid molecules may
CC also be used for generating genetically modified non-human animals and
CC for obtaining site specific gene modification in cell lines.
XX
SQ Sequence 2312 BP; 765 A; 360 C; 414 G; 773 T; 0 other;

Query Match 26.6%; Score 190.2; DB 21; Length 2312;
Best Local Similarity 56.0%; Pred. No. 5.9e-45;
Matches 407; Conservative 0; Mismatches 308; Indels 12; Gaps 2;

```
Qy      1 atgaggtctgacaagtcagctttggtatttctgctcctgcagctcttctgt---gttggc 57
Db    699 aggatgtctctgaaatggacgtcagtctttctgctgatacagctcagttgttactttagc 758

Qy     58 tgtggattctgtgggaaagtcctggtgtggccctgtgacatgagccattggcttaatgtc 117
Db    759 tctggaagctgtggaaaggtgctagtgtggcccacagaatacagccattggataaatatg 818

Qy    118 aaggtcattctagaagagctcatagtgagaggccatgaggtaacagtattgactcactca 177
Db    819 aagacaatcctggaagagcttgttcagaggggtcatgaggtgactgtgttgacatcttcg 878

Qy    178 aagccttcgttaattgactacaggaagccttctgcattgaaatttgaggtggtccatatg 237
Db    879 gcttctactcttgtcaatgccagtaaatcatctgctattaaattagaagtttatcctaca 938

Qy    238 cc---------acaggacagaacagaagaaaatgaaatatatgttgacctagctctgaat 288
Db    939 tctttaactaaaaatgatttggaagattctcttctgaaaattctcgatagatggatatat 998

Qy    289 gtcttgccaggcttatcaacctggcaatcagttataaaattaaatgatttttttgttgaa 348
Db    999 ggtgtttcaaaaaatacattttggtcatatttttcacaattacaagaattgtgttgggaa 1058

Qy    349 ataagaggaactttaaaaatgatgtgtgagagctttatctacaatcagacacttatgaag 408
Db   1059 tattatgactacagtaacaagctctgtaaagatgcagttttgaataagaaacttatgatg 1118

Qy    409 aagctacaggaaaccaactacgatgtaacgcttatagaccctgtgattccccgtggagac 468
Db   1119 aaactacaagagtcaaagtttgatgtcattctggcagatgcccttaatccctgtggtgag 1178

Qy    469 ctgatggctgagttgcttccagtccctttttgtgctcacacttagaacttctctaagaggc 528
Db   1179 ctactggctgaactatttaacataccctttctgtacagtcttcgattctctgttggctac 1238

Qy    529 aatatggagcgaagctgtgggaaacttccagctccactttcctatgtacctgtgcctatg 588
Db   1239 acatttgagaagaatggtggaggatttctgttccctccttcctatgtacctgttgttatg 1298

Qy    589 acaggactaacagacagaatgacctttctggaaagagtaaaaaattcaatgctttcagtt 648
Db   1299 tcagaattaagtgatcaaatgattttcatggagaggataaaaaatatgatacatatgctt 1358

Qy    649 ttgttccacttctggattcaggattacgactatcatttttgggaagagttttatagtaag 708
Db   1359 tattttgacttttggtttcaaatttatgatctgaagaagtgggaccagttttatagtgaa 1418

Qy    709 gcattag 715
Db   1419 gttctag 1425
```

```
RESULT   4
AAZ95193
ID   AAZ95193 standard; DNA; 1323 BP.
XX
AC   AAZ95193;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UGT2B4 exon 1 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B4; UGT2B4; polymorphism; metabolism; SNPs;
KW   drug interaction; detect; human; single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions
XX
PS   Example 1; Page 31; 72pp; English.
XX
CC   This sequence represents the nucleotide sequence of exon 1 of the human
CC   UDP-glucuronosyltransferase 2B4 (UGT2B4) gene.
CC   UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse
CC   the glucuronic acid conjugation of a wide range of endogenous and
CC   exogenous substrates. The UGT2B gene subfamily encode steroid
CC   metabolizing isoforms in the liver. Alteration of the expression or
CC   function of UGTs may effect drug metabolism. The invention relates to
CC   non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC   sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC   can be used to detect altered UGT2B metabolism of a substrate in an
CC   individual. The nucleic acid molecules comprising a human UGT2B sequence
CC   polymorphism can be used in screening assays for genotyping individuals,
CC   also to predict their rate of metabolism of UGT2B substrate, potential
CC   drug-drug interactions and adverse side effects. The polymorphisms can be
CC   used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC   linkage related to phenotypic variation in activity or expression of
CC   UGT2B protein. The polymorphism containing nucleic acid molecules may
CC   also be used for generating genetically modified non-human animals and
CC   for obtaining site specific gene modification in cell lines.
XX
SQ   Sequence 1323 BP; 403 A; 225 C; 253 G; 442 T; 0 other;

  Query Match             26.1%;  Score 186.8;  DB 21;  Length 1323;
  Best Local Similarity   55.7%;  Pred. No. 4.4e-44;
  Matches  403;  Conservative    0;  Mismatches  312;  Indels    9;  Gaps    2;

Qy       1 atgaggtctgacaagtcagctttggtatttctgctcctgcagctcttctgt---gttggc 57
Db     174 aggatgtctatgaaatggacttcagctcttctgctgatacagctgagctgttactttagc 233

Qy      58 tgtggattctgtgggaaagtcctggtgtggccctgtgacatgagccattggcttaatgtc 117
Db     234 tctgggagttgtggaaaggtgctggtgtggcccacagaattcagccactggatgaatata 293

Qy     118 aaggtcattctagaagagctcatagtgagaggccatgaggtaacagtattgactcactca 177
Db     294 aagacaatcctggatgaacttgtccagagaggtcatgaggtgactgtattggcatcttca 353

Qy     178 aagccttcgttaattgactacaggaagccttctgcattg[illegible]atttgaggtggtccatatg 237
Db     354 gcttccatttctttcgatcccaacagcccatctactct[illegible]atttgaagtttatcctgta 413

Qy     238 ccacaggacagaacagaagaaaatgaaatatttgttgac[illegible]agctctga------atgtc 291
Db     414 tctttaactaaaactgagtttgaggatattatcaagcag[illegible]ggttaagagatgggcagaa 473

Qy     292 ttgccaggcttatcaacctggcaatcagttataaaattaa[illegible]gatttttttgttgaaata 351
Db     474 cttccaaaagacacattttggtcatatttttcacaagtac[illegible]agaaatcatgtggacattt 533

Qy     352 agaggaactttaaaaatgatgtgtgagagctttatctaca[illegible]tcagacacttatgaagaag 411
Db     534 aatgacatacttagaaagttctgtaaggatatagtttca[illegible]taagaaacttatgaagaaa 593

Qy     412 ctacaggaaaccaactacgatgtaacgcttatagaccctg[illegible]gattccccgtggagacctg 471
Db     594 ctacaggagtcaagatttgatgttgttcttgcagatgctg[illegible]tttcccccttttggtgagctg 653

Qy     472 atggctgagttgcttccagtccctttttgtgctcacactta[illegible]aacttctctaagaggcaat 531
Db     654 ctggccgagttacttaaaatacccctttgtctacagcctc[illegible]cttctctcctggctacgca 713

Qy     532 atggagcgaagctgtgggaaacttccagctccactttcctatgtacctgtgcctatgaca 591
Db     714 attgaaaagcatagtggaggacttctgttccctccttcctatgtgcctgttgttatgtca 773

Qy     592 ggactaacagacagaatgacctttctggaaagagtaaaaa[illegible]ttcaatgctttcagttttg 651
Db     774 gaactaagtgaccaaatgacttttcatagagagggtaaaaa[illegible]tatgatctatgtgctttat 833

Qy     652 ttccacttctggattcaggattacgactatcatttttggg[illegible]agagttttatagtaaggca 711
Db     834 tttgaattttggttccaaatatttgacatgaagaagtgg[illegible]tcagttctacagtgaagtt 893

Qy     712 ttag 715
Db     894 ctag 897


RESULT   5
AAZ95199
ID   AAZ95199 standard; DNA; 2092 BP.
XX
AC   AAZ95199;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UDP-glucuronosyltransferase 2B4 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B4; UGT2B4; polymorphism; metabolism; SNPs;
KW   drug interaction; detect; human; single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
DR   P-PSDB; AAY78933.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
```

```
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions -
XX
PS   Disclosure; Page 34-36; 72pp; English.
XX
CC   This sequence represents the human UDP-glucuronosyltransferase 2B4
CC   (UGT2B4) gene. UDP-glucuronosyltransferase (UGTs) are a family of
CC   enzymes that catalyse the glucuronic acid conjugation of a wide range of
CC   endogenous and exogenous substrates. The UGT2B gene subfamily encode
CC   steroid metabolizing isoforms in the liver. Alteration of the expression
CC   or function of UGTs may effect drug metabolism. The invention relates to
CC   non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC   sequence polymorphisms (see AAZ95051-Z95110). Probes which detect the
CC   UGT2B locus polymorphisms can be used to detect altered UGT2B metabolism
CC   of a substrate in an individual. The nucleic acid molecules comprising a
CC   human UGT2B sequence polymorphism can be used in screening assays for
CC   genotyping individuals, also to predict their rate of metabolism of
CC   UGT2B substrate, potential drug-drug interactions and adverse side
CC   effects. The polymorphisms can be used as single nucleotide polymorphisms
CC   (SNPs) for detecting genetic linkage related to phenotypic variation in
CC   activity or expression of UGT2B protein. The polymorphism containing
CC   nucleic acid molecules may also be used for generating genetically
CC   modified non-human animals and for obtaining site-specific gene
CC   modification in cell lines.
XX
SQ   Sequence 2092 BP; 639 A; 398 C; 438 G; 617 T; 0 other;

  Query Match           26.1%;  Score 186.8;  DB 21;  Length 2092;
  Best Local Similarity  55.7%;  Pred. No. 5.4e-44;
  Matches  403;  Conservative    0;  Mismatches  312;  Indels    9;  Gaps    2;

Qy      1 atgaggtctgacaagtcagctttggtatttctgctcctgcagctcttctgt---gttggc 57
          | || ||||   || |   |||  |   |||||||  | |||||   ||||    || ||
Db     35 aggatgtctatgaaatggacttcagctcttctgctgatacagctgagctgttacttagc 94

Qy     58 tgtggattctgtgggaaagtcctggtgtggccctgtgacatgagccattggcttaatgtc 117
          | |||    ||||| || || ||||||||||||   ||  | ||||| ||| | ||| |
Db     95 tctgggagttgtggaaaggtgctggtgtggcccacagaattcagccactggatgaatata 154

Qy    118 aaggtcattctagaagagctcatagtgagaggccatgaggtaacagtattgactcactca 177
          |||   || || || || ||  |   |||||| |||||||| || ||||||  |    |||
Db    155 aagacaatcctggatgaacttgtccagagaggtcatgaggtgactgtattggcatcttca 214

Qy    178 aagccttcgttaattgactacaggaagccttctgcattgaaatttgaggtggtccatatg 237
              |   | ||   ||  |  || ||| |  | ||||||| ||    | | |
Db    215 gcttccatttctttcgatcccaacagcccatctactcttaaatttgaagtttatcctgta 274

Qy    238 ccacaggacagaacagaagaaaatgaaatatttgttgacctagctctga------atgtc 291
           |       | ||| ||     | || ||  |     | || | |  ||       |
Db    275 tctttaactaaaactgagtttgaggatattatcaagcagctggttaagagatgggcagaa 334

Qy    292 ttgccaggcttatcaacctggcaatcagttataaaattaaatgatttttttgttgaaata 351
           | |||       ||   |||  ||   ||  | || || | ||  |  |      | |
Db    335 cttccaaaagacacattttggtcatatttttcacaagtacaagaaatcatgtggacattt 394

Qy    352 agaggaactttaaaaatgatgtgtgagagctttatctacaatcagacacttatgaagaag 411
          |  |  |   | | || | | ||| ||    |  | |  ||| ||| ||||||||||||
Db    395 aatgacatacttagaaagttctgtaaggatatagtttcaaataagaaacttatgaagaaa 454

Qy    412 ctacaggaaaccaactacgatgtaacgcttatagaccctgtgattccccgtggagacctg 471
          ||||||||  | |  |  |||||    |||  |||  ||||  | |||  ||| || |||
Db    455 ctacaggagtcaagatttgatgttgttcttgcagatgctgttttccccttggtgagctg 514

Qy    472 atggctgagttgcttccagtccctttttgtgctcacacttagaacttctctaagaggcaat 531
           |||| ||||| |||  | | || |||||   ||  ||  |    ||||   |  |
Db    515 ctggccgagttacttaaaataccctttgtctacagcctccgcttctctcctggctacgca 574

Qy    532 atggagcgaagctgtgggaaacttccagctccactttcctatgtacctgtgcctatgaca 591
          || ||       ||||  |||||    || | |||||||| |||||   |||| ||
Db    575 attgaaaagcatagtggaggacttctgttccctccttcctatgtgcctgttgttatgtca 634

Qy    592 ggactaacagacagaatgacctttctggaaagagtaaaaaattcaatgctttcagttttg 651
          | ||||  |||  |||||| ||  | || || ||||||||   ||   |    |||
Db    635 gaactaagtgaccaaatgactttcatagagagggtaaaaa-tatgatctatgtgctttat 694

Qy    652 ttccacttctggattcaggattacgactatcatttttgggaagagttttatagtaaggca 711
          ||  | || ||| | ||    |  |||    |   ||||| |||| || ||| | |
Db    695 tttgaattttggttccaaatatttgacatgaagaagtggg-tcagttctacagtgaagtt 754

Qy    712 ttag 715
           |||
Db    755 ctag 758


RESULT   6
AAC65396
ID   AAC65396 standard; cDNA; 1650 BP.
XX
AC   AAC65396;
XX
DT   13-FEB-2001  (first entry)
XX
DE   Human carbohydrate-modifying enzyme cDNA Incyte ID No: 2912330CB1.
XX
KW   Human; carbohydrate-modifying enzyme; CME; antidiabetic;
KW   immunosuppressive; anti-HIV; antiinflammatory; antianaemic;
KW   antiasthmatic; antiarteriosclerotic; antithyroid; hepatotropic;
KW   nephrotropic; antigout; thyromimetic; neuroprotective; osteopathic;
KW   antiarthritic; antipsoriatic; uropathic; ophthalmological;
KW   dermatological; antiulcer; cytostatic; viricide; antibacterial;
KW   fungicide; protozoacide; tranquiliser; vulnerary; diabetes;
KW   autoimmune disorder; inflammatory disorder; infection; ss.
XX
OS   Homo sapiens.
XX
PN   WO200063351-A2.
XX
PD   26-OCT-2000.
XX
PF   20-APR-2000; 2000WO-US10882.
XX
PR   21-APR-1999;   99US-0130383.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Lal P,  Yue H,  Tang YT,  Hillman JL,  Baughn MR,  Yang J;
XX
DR   WPI; 2000-672729/65.
DR   P-PSDB; AAB28677.
XX
PT   Novel carbohydrate modifying enzyme polypeptides and polynucleotides
PT   for diagnosis, treatment, and prevention of carbohydrate metabolism
PT   disorders, autoimmune/inflammatory disorders, and cancer -
XX
PS   Claim 4; Page 75; 75pp; English.
XX
CC   The present cDNA sequence encodes a human carbohydrate-modifying enzyme
CC   (CME). CME polynucleotides and polypeptides are useful for treating and
CC   diagnosing diseases associated with CME such as diabetes,
CC   autoimmune/inflammatory disorders such as AIDS, Addison's disease,
CC   adult respiratory distress syndrome, allergies, anaemia, asthma,
CC   atherosclerosis, autoimmune thyroiditis, bronchitis, cholocystitis,
CC   contact dermatitis, Crohn's disease, emphysema, erythroblastosis fetalis,
CC   glomerulonephritis, Good pasture's syndrome, gout, Grave's disease,
CC   Hashimoto's thyroiditis, multiple sclerosis, myasthenia gravis,
CC   osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,
CC   Reiter's syndrome, arthritis, scleroderma, sjogren's syndrome, systemic
CC   lupus erythematosus, ulcerative colitis, uveitis, Werner syndrome,
CC   complications of cancer, haemodialysis, and extracorporeal circulation,
CC   viral, bacterial, fungal parasitic, protozoal, and helminthic infections,
CC   trauma, or cancer. CME, or its catalytic or immunogenic fragment, is
CC   useful for drug screening.
XX
SQ   Sequence 1650 BP; 489 A; 330 C; 354 G; 477 T; 0 other;
```

```
Query Match             26.0%;  Score 186.2;  DB 21;  Length 1650;
Best Local Similarity   55.4%;  Pred. No. 7.2e-44;
Matches  384;  Conservative    0;  Mismatches  303;  Indels    6;  Gaps    1;

Qy      29 ttctgctcctgcagctcttctgtgttggctgtggattctgtgggaaagtcctggtgtggc 88
           | ||| | | || |  ||  |   || ||| |||    ||||| || || ||||||||||
Db      63 tcctgatacagctgagctgttactttagctctgggagttgtggaaaggtgctggtgtggc 122

Qy      89 cctgtgacatgagccattggcttaatgtcaaggtcattctagaagagctcatagtgagag 148
           ||   ||  | ||||| ||| | ||| | |||   || || || || ||  |   |||||
Db     123 ccacagaattcagccactggatgaatataaagacaatcctggatgaacttgtccagagag 182

Qy     149 gccatgaggtaacagtattgactcactcaaagccttcgttaattgactacaggaagcctt 208
           | |||||||| || |||||| |    |||     |    |  | ||   ||  |  || |
Db     183 gtcatgaggtgactgtattggcatcttcagcttccatttctttcgatcccaacagcccat 242

Qy     209 ctgcattgaaatttgaggtggtccatatgccacaggacagaacagaagaaaatgaaatat 268
           || |  | |||||||| ||    | | |  |       | ||| ||     | || ||
Db     243 ctactcttaaatttgaagtttatcctgtatctttaactaaaactgagtttgaggatatta 302

Qy     269 ttgttgacctagctctga------atgtcttgccaggcttatcaacctggcaatcagtta 322
           |     | || | |  ||       |   | |||       ||   |||  ||   ||
Db     303 tcaagcagctggttaagagatgggcagaacttccaaaagacacatttggtcatatttttt 362

Qy     323 taaaattaaatgatttttttgttgaaataagaggaactttaaaaatgatgtgtgagagct 382
           | || || | ||  | |       | | |  |  |  | || | | ||| ||
Db     363 cacaagtacaagaaatcatgtggacatttaatgacatacttagaaagttctgtaaggata 422

Qy     383 ttatctacaatcagacacttatgaagaagctacaggaaaccaactacgatgtaacgctta 442
           |  | |  ||| ||| ||||||||||||| |||||||  | | . |  |||||    |||
Db     423 tagtttcaaataagaaacttatgaagaaactacaggagtcaagatttgatgttgttcttg 482

Qy     443 tagaccctgtgattccccgtggagacctgatggctgagttgcttccagtccctttttgtgc 502
           |||  ||||  | |||  ||| || ||| |||| ||||| |||  | |. || |||||
Db     483 cagatgctgttttccccttggtgagctgctggccgagttacttaaaataccctttgtct 542

Qy     503 tcacacttagaacttctctaagaggcaatatggagcgaagctgtgggaaacttccagctc 562
           ||  ||  |    ||||   |   |  || ||       ||||   |||||     |
Db     543 acagcctccgcttctctcctggctacgcaattgaaaagcatagtggaggacttctgttcc 602

Qy     563 cactttcctatgtacctgtgcctatgacaggactaacagacagaatgacctttctggaaa 622
           | | ||||||||| |||||   |||| ||| |||||  |||  |||||| ||  | || |
Db     603 ctccttcctatgtgcctgttgttatgtcagaactaagtgaccaaatgactttcatagaga 662

Qy     623 gagtaaaaaattcaatgctttcagttttgttccacttctggattcaggattacgactatc 682
           | |||||||||   ||   |    |||  ||  | || ||| | ||    |  |||
Db     663 gggtaaaaaatatgatctatgtgctttattttgaattttggttccaaatatttgacatga 722

Qy     683 atttttgggaagagttttatagtaaggcattag 715
           |    |||||  |||| || ||| | |   |||
Db     723 agaagtgggatcagttctacagtgaagttctag 755


RESULT   7
AAV15900
ID   AAV15900 standard; cDNA; 2107 BP.
XX
AC   AAV15900;
XX
DT   26-MAY-1998  (first entry)
XX
DE   Uridine diphospho-glucuronosyltransferase 2B17 (UGT2B17) encoding cDNA.
XX
KW   Uridine diphospho-glucuronosyltransferase 2B17; UGT2B17; catalyse;
KW   androsterone; androsterone-glucuronic acid; androgen; enzyme; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..51
FT                   /*tag=  a
FT   CDS             52..1644
FT                   /*tag=  b
FT                   /product= "UGTB17 enzyme"
FT   3'UTR           1645..2107
FT                   /*tag=  c
XX
PN   WO9744466-A1.
XX
PD   27-NOV-1997.
XX
PF   16-MAY-1997;    97WO-CA00328.
XX
PR   17-MAY-1996;    96US-0649319.
XX
PA   (ENDO-) ENDORECHERCHE INC.
XX
PI   Beaulieu M,  Belanger A,  Hum DW,  Levesque E;
XX
DR   WPI; 1998-018520/02.
DR   P-PSDB; AAW47126.
XX
PT   DNA encoding uridine di:phospho:glucuronosyl:transferase 2B17 -
PT   which catalyses conversion of androsterone to
PT   androsterone-glucuronic acid
XX
PS   Claim 15; Pages 4-6; 53pp; English.
XX
CC   This cDNA encodes an enzyme uridine di-phosphoglucuronosyltransferase
CC   2B17 (UGT2B17). This novel enzyme catalyses the conversion of
CC   androsterone to androsterone-glucuronic acid. The UGT2B17 can be used to
CC   detect anti-UGT2B17 antibodies. The antibody can be used to detect a
CC   localised concentration of UGT2B17 or an alteration in androgen activity.
CC   The UGT2B17 can also be used to alter the concentration of an androgenic
CC   compound in a tissue, specifically dihydrotestosterone. An isolated
CC   nucleotide sequence comprising at least 30 consecutive nucleotides from
CC   the coding region of the 2107 base pair sequence, or its complement can
CC   be used to block the synthesis of UGT2B17, e.g. an expression disrupting
CC   sense or antisense fragment, or as a probe for a UGT2B17 coding sequence.
XX
SQ   Sequence 2107 BP; 657 A; 382 C; 424 G; 644 T; 0 other;


Query Match             25.0%;  Score 179;  DB 19;  Length 2107;
Best Local Similarity   55.0%;  Pred. No. 9.5e-42;
Matches  400;  Conservative    0;  Mismatches  315;  Indels   12;  Gaps    2;

Qy       1 atgaggtctgacaagtcagctttggtatttctgctcctgcagctcttctgt---gttggc 57
           | || ||||   || |     |  || |||||||| ||||||||   |||    || ||
Db      49 aggatgtctctgaaatggatgtcagtctttctgctgatgcagctcagttgttactttagc 108

Qy      58 tgtggattctgtgggaaagtcctggtgtggccctgtgacatgagccattggcttaatgtc 117
           | |||    ||||| || || |||||||||||||   ||  ||||||||| | ||| |
Db     109 tctgggagttgtggaaaggtgctggtgtggcccacagaatacagccattggataaatatg 168

Qy     118 aaggtcattctagaagagctcatagtgagaggccatgaggtaacagtattgactcactca 177
           |||   || || |||||||||  |   ||| || |||||||| |  || |||||    ||
Db     169 aagacaatcctggaagagcttgttcagaggggtcatgaggtgattgtgttgacatcttcg 228

Qy     178 aagccttcgttaattgactacaggaagccttctgcattgaaatttgaggtggtccatatg 237
           ||    |  |  |   ||| ||  | |||||  | ||||| || ||    | ||
Db     229 gcttctattcttgtcaatgccagtaaatcatctgctattaaattagaagtttatcctaca 288

Qy     238 ccacaggacagaacagaagaaaatgaaatatttt--------gttgacctagctctgaat 288
           |     | ||  ||     | ||  | |||          | ||   |       ||
Db     289 tctttaactaaaaatgatttggaagatttttttatgaaaatgttcgatagatggacatat 348

Qy     289 gtcttgccaggcttatcaacctggcaatcagttataaaatttaaatgatttttttgttgaa 348
           |  ||       ||   |||  ||   ||  | || || | || || | |   |||
Db     349 agtatttcaaaaaatacattttggtcatatttttcacaactacaagaattgtgttgggaa 408

Qy     349 ataagaggaactttaaaaatgatgtgtgagagctttatctacaatcagacacttatgaag 408
           |    |   | || | | |||||        | |  ||  ||| ||||||||
Db     409 tattctgactataatataaagctctgtgaagatgcagttttgaacaagaaacttatgaga 468
```

```
Qy    409 aagctacaggaaaccaactactacgatgtaacgcttatagaccctgtgattccccgtggagac 468
          || ||||| ||  | || |  |||||    ||   |||  | || | |||| |||| ||
Db    469 aaactacaagagtcaaaatttgatgtccttctggcagatgccgttaatccctgtggtgag 528

Qy    469 ctgatggctgagttgcttccagtccctttttgtgctcacacttagaaacttctctaagaggc 528
          ||| |||||||  | |||    | || ||| ||  ||  ||  |    ||| |  |   |
Db    529 ctgctggctgaactacttaacataccctttctgtacagtctccgcttctctgttggctac 588

Qy    529 aatatggagcgaagctgtgggaaacttccagctccactttcctatgtacctgtgcctatg 588
          |   | |||   |   ||||   | |||     || | ||||||||||||||||   ||||
Db    589 acagttgagaagaatggtggaggatttctgttccctccttcctatgtacctgttgttatg 648

Qy    589 acaggactaacagacagaatgacctttctggaaagagtaaaaaattcaatgctttcagtt 648
           ||| | |||  ||   |||||  ||  |||| ||  |||||||||   ||   |    ||
Db    649 tcagaattaagtgatcaaatgattttcatggagaggataaaaaatatgatatatatgctt 708

Qy    649 ttgttccacttctggattcaggattacgactatcatttttgggaagagttttatagtaag 708
          |  ||  |||| ||| |||| |  || ||     |    |||||  ||||||||||| |
Db    709 tattttgacttttggtttcaagcatatgatctgaagaagtgggaccagttttatagtgaa 768

Qy    709 gcattag 715
          |   |||
Db    769 gttctag 775


RESULT   8
AAZ95201
ID   AAZ95201 standard; DNA; 1686 BP.
XX
AC   AAZ95201;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UGT2B7 exon 1 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B7; UGT2B7; polymorphism; metabolism; SNPs;
KW   drug interaction; detect; human; single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions  -
XX
PS   Example 2; Page 45; 72pp; English.
XX
CC   This sequence represents the nucleotide sequence of exon 1 of the human
CC   UDP-glucuronosyltransferase 2B7 (UGT2B7) gene.
CC   UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse
CC   the glucuronic acid conjugation of a wide range of endogenous and
CC   exogenous substrates. The UGT2B gene subfamily encode steroid
CC   metabolizing isoforms in the liver. Alteration of the expression or
CC   function of UGTs may effect drug metabolism. The invention relates to
CC   non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC   sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC   can be used to detect altered UGT2B metabolism of a substrate in an
CC   individual. The nucleic acid molecules comprising a human UGT2B sequence
CC   polymorphism can be used in screening assays for genotyping individuals,
CC   also to predict their rate of metabolism of UGT2B substrate, potential
CC   drug-drug interactions and adverse side effects. The polymorphisms can be
CC   used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC   linkage related to phenotypic variation in activity or expression of
CC   UGT2B protein. The polymorphism containing nucleic acid molecules may
CC   also be used for generating genetically modified non-human animals and
CC   for obtaining site specific gene modification in cell lines.
XX
SQ   Sequence 1686 BP; 548 A; 286 C; 295 G; 557 T; 0 other;


  Query Match             24.1%;  Score 172.4;  DB 21;  Length 1686;
  Best Local Similarity   54.4%;  Pred. No. 6.9e-4[illegible];
  Matches  394;  Conservative    0;  Mismatches  321;  Indexels    9;  Gaps    2;

Qy      1 atgaggtctgacaagtcagctttggtatttctgctcctg[illegible]gct---cttctgtgttggc 57
            | || |||||  || |   |||  ||| || ||||  |  ·  ||   ||| ||  || ||
Db    403 aggatgtctgtgaaatggacttcagtaattttgctaata[illegible]actgagcttttgctttagc 462

Qy     58 tgtggattctgtgggaaagtcctggtgtggccctgtgacatgagccattggcttaatgtc 117
          | |||    ||||| || || |||||||||  |    ||    |||||||||  | ||| |
Db    463 tctgggaattgtggaaaggtgctggtgtgggcagcagaatacagccattggatgaatata 522

Qy    118 aaggtcattctagaagagctcatagtgagaggccatgaggtaacagtattgactcactca 177
          |||   || || || ||||| ||   |||||| |||||||| || ||| || |    |||
Db    523 aagacaatcctggatgagcttattcagagaggtcatgaggtgactgtactggcatcttca 582

Qy    178 aagccttcgttaattgactacaggaagccttctgcattgaaatttgaggtggtccatatg 237
              |  | ||||   ||  ||  | || ||  | ||| ||||  |    |  | |
Db    583 gcttccattctttttgatcccaacaactcatccgctcttaaaattgaaatttatcccaca 642

Qy    238 ccacaggacagaacagaagaaaatgaaatatttgttgacctagctctga------atgtc 291
              |       | ||| ||     |  |  |  |  | | |    |  ||       | |
Db    643 tctttaactaaaactgagttggagaatttcatcatgcaacagattaagagatggtcagac 702

Qy    292 ttgccaggcttatcaacctggcaatcagttataaaattaaatgatttttttgttgaaata 351
           | |||       ||   |||  ||   ||  | || || | ||  |  |      | |
Db    703 cttccaaaagatacattttggttatatttttcacaagtacaggaaatcatgtcaatattt 762

Qy    352 agaggaactttaaaaatgatgtgtgagagctttatctacaatcagacacttatgaagaag 411
           | |  |     | || | | ||| |      |  | |  ||| ||| | |||||| ||
Db    763 ggtgacataactagaaagttctgtaaagatgtagtttcaaataagaaatttatgaaaaaa 822

Qy    412 ctacaggaaaccaactacgatgtaacgcttatagaccctgtgattccccgtggagacctg 471
           |||| ||  | |  |  || || |   ||  |||  || |  ||||| || | || |||
Db    823 gtacaagagtcaagatttgacgtcatttttgcagatgctatttttccctgtagtgagctg 882

Qy    472 atggctgagttgcttccagtccctttttgtgctcacacttagaaacttctctaagaggcaat 531
           |||||||| |  ||    | || ||||||  ||  || ||    ||||   |   || |
Db    883 ctggctgagctatttaacataccctttgtgtacagtctcagcttctctcctggctacact 942

Qy    532 atggagcgaagctgtgggaaacttccagctccactttcctatgtacctgtgcctatgaca 591
           | ||        ||||   | ||      || | |||||| ||||||||   |||| ||
Db    943 tttgaaaagcatagtggaggatttatttttccctccttcctacgtacctgttgttatgtca 1002

Qy    592 ggactaacagacagaatgacctttctggaaagagtaaaaaattcaatgctttcagttttg 651
          | | |||| ||   ||||||  ||  |||| || ||||||  |   ||   |    |||
Db   1003 gaattaactgatcaaatgactttcatggagagggtaaaa[illegible]tatgatctatgtgctttac 1062

Qy    652 ttccacttctggattcaggattacgactatcatttttg[illegible]agagttttatagtaaggca 711
           ||  |||| ||| |  |    |  |||    |    |||[illegible]  ||||||||||| | |
Db   1063 tttgacttttggttcgaaatatttgacatgaagaagtgg[illegible]atcagttttatagtgaagtt 1122

Qy    712 ttag 715
           |||
Db   1123 ctag 1126


RESULT   9
AAZ95200
ID   AAZ95200 standard; DNA; 1854 BP.
XX
AC   AAZ95200;
XX
```

DT 05-JUN-2000 (first entry)
XX
DE Human UDP-glucuronosyltransferase 2B7 nucleotide sequence.
XX
KW UDP-glucuronosyltransferase 2B7; UGT2B7; polymorphism; metabolism; SNPs;
KW drug interaction; detect; human; single nucleotide polymorphism; ds.
XX
OS Homo sapiens.
XX
PN WO200006776-A1.
XX
PD 10-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US16675.
XX
PR 28-JUL-1998; 98US-0094391.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Galvin M, Miller A, Penny L, Riedy M;
XX
DR WPI; 2000-195321/17.
DR P-PSDB; AAY78934.
XX
PT Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT genotyping individuals to predict rate of metabolism of substrates and
PT for identifying potential drug interactions -
XX
PS Disclosure; Page 41-44; 72pp; English.
XX
CC This sequence represents the human UDP-glucuronosyltransferase 2B7
CC (UGT2B7) gene. UDP-glucuronosyltransferase (UGTs) are a family of
CC enzymes that catalyse the glucuronic acid conjugation of a wide range of
CC endogenous and exogenous substrates. The UGT2B gene subfamily encode
CC steroid metabolizing isoforms in the liver. Alteration of the expression
CC or function of UGTs may effect drug metabolism. The invention relates to
CC non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC sequence polymorphisms (see AAZ95051-Z95110). Probes which detect the
CC UGT2B locus polymorphisms can be used to detect altered UGT2B metabolism
CC of a substrate in an individual. The nucleic acid molecules comprising a
CC human UGT2B sequence polymorphism can be used in screening assays for
CC genotyping individuals, also to predict their rate of metabolism of
CC UGT2B substrate, potential drug-drug interactions and adverse side
CC effects. The polymorphisms can be used as single nucleotide polymorphisms
CC (SNPs) for detecting genetic linkage related to phenotypic variation in
CC activity or expression of UGT2B protein. The polymorphism containing
CC nucleic acid molecules may also be used for generating genetically
CC modified non-human animals and for obtaining site specific gene
CC modification in cell lines.
XX
SQ Sequence 1854 BP; 572 A; 338 C; 392 G; 552 T; 0 other;

Query Match 24.1%; Score 172.4; DB 21; Length 1854;
Best Local Similarity 54.4%; Pred. No. 7.2e-40;
Matches 394; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

```
Qy      1 atgaggtctgacaagtcagctttggtatttctgctcctgcagct---cttctgtgttggc 57
          | || |||||  || |   |||  ||| || ||||  | || ||   ||| ||  || ||
Db     12 aggatgtctgtgaaatggacttcagtaattttgctaatacaactgagcttttgctttagc 71

Qy     58 tgtggattctgtgggaaagtcctggtgtggccctgtgacatgagccattggcttaatgtc 117
          | |||    ||||| || || |||||||||| |    ||    |||||||||| | ||| |
Db     72 tctgggaattgtggaaaggtgctggtgtgggcagcagaatacagccattggatgaatata 131

Qy    118 aaggtcattctagaagagctcatagtgagaggccatgaggtaacagtattgactcactca 177
          |||   || || || ||||| ||   |||||| |||||||| || ||| || | |   |||
Db    132 aagacaatcctggatgagcttattcagagaggtcatgaggtgactgtactggcatcttca 191

Qy    178 aagccttcgttaattgactacaggaagccttctgcattgaaatttgaggtggtccatatg 237
            |    | ||||   ||  ||  | || ||  | ||| |||| |    |  |
Db    192 gcttccattctttttgatcccaacaactcatccgctcttaaaattgaaatttatcccaca 251

Qy    238 ccacaggacagaacagaagaaaatgaaatatttgttgacc agctctga------atgtc 291
          |       | ||| ||     |  |  |  |  | | |    |  ||       | |
Db    252 tctttaactaaaactgagttggagaatttcatcatgcaac attaagagatggtcagac 311

Qy    292 ttgccaggcttatcaacctggcaatcagttataaaattaa tgatttttttgttgaaata 351
          | |||       ||   |||  ||  ||  | || ||| | ||  |  |      | |
Db    312 cttccaaaagatacattttggttatatttttcacaagtac ggaaatcatgtcaatattt 371

Qy    352 agaggaactttaaaaatgatgtgtgagagctttatctacaatcagacacttatgaagaag 411
          | |  |     | || | | ||| |     |  | |  ||| ||| | ||||||| ||
Db    372 ggtgacataactagaaagttctgtaaagatgtagtttcaaataagaaatttatgaaaaaa 431

Qy    412 ctacaggaaaccaactacgatgtaacgcttatagaccctgtgattccccgtggagacctg 471
          |||| ||  | |  |  || || |   ||  |||  || |  ||||  || | || |||
Db    432 gtacaagagtcaagatttgacgtcatttttgcagatgctatttttccctgtagtgagctg 491

Qy    472 atggctgagttgcttccagtccctttttgtgctcacacttagaacttctctaagaggcaat 531
          |||||||| |  ||    | || ||||||  ||  || ||    ||||   |   || |
Db    492 ctggctgagctatttaacataccctttgtgtacagtctcagcttctctcctggctacact 551

Qy    532 atggagcgaagctgtgggaaacttccagctccactttcct tgtacctgtgcctatgaca 591
          | ||        ||||   | ||       || | |||||  ||||||||   |||| ||
Db    552 tttgaaaagcatagtggaggatttattttccctcctttcc cgtacctgttgttatgtca 611

Qy    592 ggactaacagacagaatgacctttctggaaagagtaaaaa ttcaatgctttcagttttg 651
          | | |||| ||   |||||| ||  |||| || |||||||||   ||   |   |||
Db    612 gaattaactgatcaaatgactttcatggagagggtaaaaa tatgatctatgtgctttac 671

Qy    652 ttccacttctggattcaggattacgactatcatttttggg agagttttatagtaaggca 711
          ||  |||| ||| |  |    |  |||    |   |||| |||||||||||| | |
Db    672 tttgacttttggttcgaaatatttgacatgaagaagtggg tcagttttatagtgaagtt 731

Qy    712 ttag 715
            |||
Db    732 ctag 735
```

RESULT 10
AAA87467
ID AAA87467 standard; DNA; 283 BP.
XX
AC AAA87467;
XX
DT 08-JAN-2001 (first entry)
XX
DE Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:391.
XX
KW Rat; phenobarbitol; carcinogenesis marker; ca cinogenesis; detection;
KW identification; carcinogenic; probe; primer; ds.
XX
OS Rattus norvegicus.
XX
PN WO200044902-A2.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US00503.
XX
PR 29-JAN-1999; 99US-0118078.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Bunch RT, Curtis SW, Rodi CP, Morris DL;
XX
DR WPI; 2000-505977/45.
XX
PT New nucleic acid encoding a carcinogenic biomarker, induced by
PT phenobarbitol treatment of rat hepatocytes, useful for identifying
PT carcinogenic compounds -
XX
PS Claim 1; Page 184; 240pp; English.
XX
CC AAA87080 to AAA87656 represent nucleic acid sequences (N1) encoding a

```
CC   carcinogenesis biomarkers. The carcinogenesis biomarkers are induced by
CC   treating rat hepatocytes with phenobarbitol. The nucleic acids are
CC   useful for identifying carcinogenic compounds. The nucleic acid molecules
CC   can be used to derive probes and/or primers for detecting or inducing
CC   carcinogenesis, respectively.
XX
SQ   Sequence 283 BP; 72 A; 57 C; 67 G; 87 T; 0 other;


  Query Match             17.3%;  Score 124;  DB 21;  Length 283;
  Best Local Similarity   67.5%;  Pred. No. 2.9e-26;
  Matches  189;  Conservative    0;  Mismatches   90;  Indels    1;  Gaps    1;

Qy     436 acgcttatagaccctgtgattccccgtggagacctgatggctgagttgcttccagtccct 495
           | | || | |||||||| |||||| ||||||| ||| |||| ||  | ||||   |||||
Db       1 atggttttggaccctgtcattccctgtggagagctggtggcagaagtacttcagatccct 60

Qy     496 tttgtgctcacacttagaacttctctaagaggcaatatggagcgaagctgtgggaaactt 555
           |||||   |||| | ||        |  |   |  ||||||  |  ||| ||  |||||
Db      61 tttgtaaacacattgaggttcagcatgggctactccatggagaaatactgcggccaactt 120

Qy     556 ccagctccactttcctatgtacctgtgcctatgacaggactaacagacagaatgacctttt 615
           |||| |||||||||| |||||||| ||   |  |   | ||||||||||   |||||||||
Db     121 ccagttccactttcgtatgtaccggt-tgtcagggtgaactaacagaccatatgacctttt 179

Qy     616 ctggaaagagtaaaaaattcaatgctttcagttttgttccacttctggattcaggattac 675
              || || || ||||||   |||||||||| | || ||  | || ||| | ||| | ||
Db     180 acagagagggtgaaaaatatgatgctttcactgttttttgagttttggctccagcaatat 239

Qy     676 gactatcatttttgggaagagttttatagtaaggcattag 715
           |||| |   || |||||  |||||||  |||||  |  |||
Db     240 gactttgcattctgggatcagttttacagtaaaactctag 279


RESULT  11
AAF58252/c
ID   AAF58252 standard; DNA; 936 BP.
XX
AC   AAF58252;
XX
DT   24-APR-2001  (first entry)
XX
DE   Oligonucleotide D1835.
XX
KW   Electron-transfer group; ETM; mismatch; genotyping;
KW   gene expression; ss.
XX
OS   Synthetic.
XX
PN   WO200107665-A2.
XX
PD   01-FEB-2001.
XX
PF   26-JUL-2000; 2000WO-US20476.
XX
PR   26-JUL-1999;   99US-0145695.
PR   17-MAR-2000; 2000US-0190259.
XX
PA   (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI   Umek RM;
XX
DR   WPI; 2001-159728/16.
XX
PT   Nucleic acids containing electron-transfer group, useful as labels in
PT   hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT   a single surface -
XX
PS   Example 6; Page 127; 159pp; English.
XX
CC   The present invention relates to a composition comprising two nucleic
CC   acids each containing an electron-transfer group (ETM) having
CC   different redox potentials. The invention is used for electronic
CC   detection of nucleic acids, especially of substitutions (mismatches)
CC   and single-nucleotide polymorphisms, e.g. for genotyping,
CC   monitoring gene expression.
XX
SQ   Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;


  Query Match             11.3%;  Score 81;  DB 22;  Length 936;
  Best Local Similarity   1.0%;  Pred. No. 1.2e-13;
  Matches    6;  Conservative  362;  Mismatches  237;  Indels    0;  Gaps    0;

Qy     110 ttaatgtcaaggtcattctagaagagctcatagtgagaggccatgaggtaacagtattga 169
           ::::: : ::  : ::: :: :: :  : ::: : : :    :: :  ::: : :::: :
Db     664 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 605

Qy     170 ctcactcaaagccttcgttaattgactacaggaagccttctgcattgaaatttgaggtgg 229
            : : : :::  |::  :::::: : :: :  ::   :: :  ::: :::::: :  :
Db     604 WWWWWWWWWWWWCWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 545

Qy     230 tccatatgccacaggacagaacagaagaaaatgaaatatttgttgacctagctctgaatg 289
           :  ::::   : :  : : :: : :: ::::: :::::::: :: :  ::| : : :::
Db     544 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWGWWWWWWWWWW 485

Qy     290 tcttgccaggcttatcaacctggcaatcagttataaaattaaatgatttttttgttgaaa 349
           : ::   :   :::: ::  :   ::: : :::::::::::::: :::::::: :: :::
Db     484 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 425

Qy     350 taagaggaactttaaaaatgatgtgtgagagctttatctacaatcagacacttatgaaga 409
           ::: :  :: ::::::::: :: : : : |   :::: :: ::: : : : :::: :: :
Db     424 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWTAAGCWWWWWWWWWWWWWWWWWWWWWW 365

Qy     410 agctacaggaaaccaactacgatgtaacgcttatagaccctgtgattccccgtggagacc 469
           :  :: :  :::  :: ::  :: :::   ::::: :   : : :::     :  : :
Db     364 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 305

Qy     470 tgatggctgagttgcttccagtccctttttgtgctcacactagaacttctctaagaggca 529
           : ::   : :|::  ::  : :  :::: :  : : : ::: :: :: : ::: :   :
Db     304 WWWWWWWWWWGWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 245

Qy     530 atatggagcgaagctgtgggaaacttccagctccacttttctatgtacctgtgcctatga 589
           ::::  :  ::  : :  ::: :: :  :  : ::: ::: :: |: :  ::: :
Db     244 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 185

Qy     590 caggactaacagacagaatgacctttctggaaagagtaaaaattcaatgctttcagttt 649
           :  : ::: : : : ::: :  ::: :  ::: : ::::::::: :::  ::: : :::
Db     184 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 125

Qy     650 tgttccacttctggattcaggattacgactatcatttttgggaagagttttatagtaagg 709
           : ::  : :: :  ::: :  :::: |: ::: ::::::   :: : ::::::: :::
Db     124 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWGWWWWWWWWWWWWWWWWWWWWWWWWWWW 65

Qy     710 catta 714
           ::::
Db      64 WWWWW 60


RESULT  12
AAF58254/c
ID   AAF58254 standard; DNA; 936 BP.
XX
AC   AAF58254;
XX
DT   24-APR-2001  (first entry)
XX
DE   Oligonucleotide D1875.
XX
KW   Electron-transfer group; ETM; mismatch; genotyping;
KW   gene expression; ss.
XX
OS   Synthetic.
XX
PN   WO200107665-A2.
XX
```

PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI; 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface -
XX
PS Example 6; Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;

Query Match 11.3%; Score 81; DB 22; Length 936;
Best Local Similarity 1.0%; Pred. No. 1.2e-13;
Matches 6; Conservative 362; Mismatches 237; Indels 0; Gaps 0;

Qy 110 ttaatgtcaaggtcattctagaagagctcatagtgagaggccatgaggtaacagtattga 169
Db 664 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 605

Qy 170 ctcactcaaagccttcgttaattgactacaggaagccttctgcattgaaatttgaggtgg 229
Db 604 WWWWWWWWWWWWCWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 545

Qy 230 tccatatgccacaggacagaacagaagaaaatgaaatatttgttgacctagctctgaatg 289
Db 544 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWGWWWWWWWW 485

Qy 290 tcttgccaggcttatcaacctggcaatcagttataaaattaaatgatttttttgttgaaa 349
Db 484 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 425

Qy 350 taagaggaactttaaaaatgatgtgtgagagctttatctacaatcagacacttatgaaga 409
Db 424 WWWWWWWWWWWWWWWWWWWWWWWWWWWWTAAGCWWWWWWWWWWWWWWWWWWWWWWWWW 365

Qy 410 agctacaggaaaccaactacgatgtaacgcttatagaccctgtgattccccgtggagacc 469
Db 364 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 305

Qy 470 tgatggctgagttgcttccagtccctttttgtgctcacacttagaacttctctaagaggca 529
Db 304 WWWWWWWWWWGWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 245

Qy 530 atatggagcgaagctgtgggaaacttccagctccactttcctatgtacctgtgcctatga 589
Db 244 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWCWWWWWWWWWWW 185

Qy 590 caggactaacagacagaatgacctttctggaaagagtaaaaaattcaatgctttcagttt 649
Db 184 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 125

Qy 650 tgttccacttctggattcaggattacgactatcatttttgggaagagttttatagtaagg 709
Db 124 WWWWWWWWWWWWWWWWWWWWWWWWWWWWGWWWWWWWWWWWWWWWWWWWWWWWWWWWW 65

Qy 710 catta 714
Db 64 WWWWW 60

RESULT 13
AAF58257/c
ID AAF58257 standard; DNA; 936 BP.
XX
AC AAF58257;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1954.
XX
KW Electron-transfer group; ETM; mismatch; genotyping;
KW gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI; 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface -
XX
PS Example 6; Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

Query Match 11.3%; Score 81; DB 22; Length 936;
Best Local Similarity 1.0%; Pred. No. 1.2e-13;
Matches 6; Conservative 362; Mismatches 237; Indels 0; Gaps 0;

Qy 110 ttaatgtcaaggtcattctagaagagctcatagtgagaggccatgaggtaacagtattga 169
Db 664 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 605

Qy 170 ctcactcaaagccttcgttaattgactacaggaagccttctgcattgaaatttgaggtgg 229
Db 604 WWWWWWWWWWWWCWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 545

Qy 230 tccatatgccacaggacagaacagaagaaaatgaaatatttgttgacctagctctgaatg 289
Db 544 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWGWWWWWWWW 485

Qy 290 tcttgccaggcttatcaacctggcaatcagttataaaattaaatgatttttttgttgaaa 349
Db 484 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 425

Qy 350 taagaggaactttaaaaatgatgtgtgagagctttatctacaatcagacacttatgaaga 409

```
Db    424 WWWWWWWWWWWWWWWWWWWWWWWWWWWWTAAGCWWWWWWWWWWWWWWWWWWWWWWWWWWWW 365

Qy    410 agctacaggaaaccaactacgatgtaacgcttatagaccctgtgattccccgtggagacc 469
          :  :: :  :::  :: ::  :: :::   ::::: :   : : :::     : : :
Db    364 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 305

Qy    470 tgatggctgagttgcttccagtccctttgtgctcacacttagaacttctctaagaggca 529
          : ::   : :|::  ::  : :   :::: :  : : : ::: :: :: : ::: :   :
Db    304 WWWWWWWWWWGWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 245

Qy    530 atatggagcgaagctgtgggaaacttccagctccactttcctatgtacctgtgcctatga 589
          :::: :   ::  : :  ::: ::  :  :  : ::: ::: :: |: :   ::: :
Db    244 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWCWWWWWWWWWW 185

Qy    590 caggactaacagacagaatgacctttctggaaagagtaaaaaattcaatgctttcagttt 649
          :  : ::: : : : ::: :  ::: :  ::: : ::::::::: :::  ::: : :::
Db    184 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 125

Qy    650 tgttccacttctggattcaggattacgactatcatttttgggaagagttttatagtaagg 709
          : ::  : :: :  ::: :  :::: |: ::: ::::::   :: : ::::::: :::
Db    124 WWWWWWWWWWWWWWWWWWWWWWWWWWGWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 65

Qy    710 catta 714
          ::::
Db     64 WWWWW 60


RESULT  14
AAF58259/c
ID   AAF58259 standard; DNA; 936 BP.
XX
AC   AAF58259;
XX
DT   24-APR-2001  (first entry)
XX
DE   Oligonucleotide D2004.
XX
KW   Electron-transfer group; ETM; mismatch; genotyping;
KW   gene expression; ss.
XX
OS   Synthetic.
XX
PN   WO200107665-A2.
XX
PD   01-FEB-2001.
XX
PF   26-JUL-2000; 2000WO-US20476.
XX
PR   26-JUL-1999;   99US-0145695.
PR   17-MAR-2000; 2000US-0190259.
XX
PA   (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI   Umek RM;
XX
DR   WPI; 2001-159728/16.
XX
PT   Nucleic acids containing electron-transfer group, useful as labels in
PT   hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT   a single surface  -
XX
PS   Example 6; Page 128; 159pp; English.
XX
CC   The present invention relates to a composition comprising two nucleic
CC   acids each containing an electron-transfer group (ETM) having
CC   different redox potentials. The invention is used for electronic
CC   detection of nucleic acids, especially of substitutions (mismatches)
CC   and single-nucleotide polymorphisms, e.g. for genotyping,
CC   monitoring gene expression.
XX
SQ   Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

  Query Match             11.3%;  Score 81;  DB 22;  Length 936;
  Best Local Similarity   1.0%;  Pred. No. 1.2e-13;
  Matches    6;  Conservative  362;  Mismatches  237;  Indels    0;  Gaps    0;

Qy    110 ttaatgtcaaggtcattctagaagagctcatagtgagagtcatgaggtaacagtattga 169
          ::::: : ::  : ::: :: :: :  : ::: : : :    :: :  ::: : :::: :
Db    664 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 605

Qy    170 ctcactcaaagccttcgttaattgactacaggaagccttcgcattgaaatttgaggtgg 229
          : : : :::  |::  :::::: : :: :  ::   :: :  ::: :::::: :  :
Db    604 WWWWWWWWWWWWCWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 545

Qy    230 tccatatgccacaggacagaacagaagaaaatgaaatatttgttgacctagctctgaatg 289
          :  ::::   : :  : : :: : :: ::::: :::::::: :: :  ::| : : :::
Db    544 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWGWWWWWWWWW 485

Qy    290 tcttgccaggcttatcaacctggcaatcagttataaaattaaatgatttttttgttgaaa 349
          : ::   :  :::: ::  :  ::: : :::::::::::::: :::::::: :: :::
Db    484 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 425

Qy    350 taagaggaactttaaaaatgatgtgtgagagctttatctacaatcagacacttatgaaga 409
          ::: :  :: ::::::::: :: : : : |   :::: :: ::: : : : :::: :: :
Db    424 WWWWWWWWWWWWWWWWWWWWWWWWWWWWTAAGCWWWWWWWWWWWWWWWWWWWWWWWWWWWW 365

Qy    410 agctacaggaaaccaactacgatgtaacgcttatagaccctgtgattccccgtggagacc 469
          :  :: :  :::  :: ::  :: :::   ::::: :   : : :::     : : :
Db    364 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 305

Qy    470 tgatggctgagttgcttccagtccctttgtgctcacacttagaacttctctaagaggca 529
          : ::   : :|::  ::  : :   :::: :  : : : ::: :: :: : ::: :   :
Db    304 WWWWWWWWWWGWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 245

Qy    530 atatggagcgaagctgtgggaaacttccagctccactttcctatgtacctgtgcctatga 589
          :::: :   ::  : :  ::: ::  :  :  : ::: ::: :: |: :   ::: :
Db    244 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWCWWWWWWWWWW 185

Qy    590 caggactaacagacagaatgacctttctggaaagagtaaaaaattcaatgctttcagttt 649
          :  : ::: : : : ::: :  ::: :  ::: : ::::::::: :::  ::: : :::
Db    184 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 125

Qy    650 tgttccacttctggattcaggattacgactatcatttttgggaagagttttatagtaagg 709
          : ::  : :: :  ::: :  :::: |: ::: ::::::   :: : ::::::: :::
Db    124 WWWWWWWWWWWWWWWWWWWWWWWWWWGWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 65

Qy    710 catta 714
          ::::
Db     64 WWWWW 60


RESULT  15
AAF58262/c
ID   AAF58262 standard; DNA; 936 BP.
XX
AC   AAF58262;
XX
DT   24-APR-2001  (first entry)
XX
DE   Oligonucleotide D2007.
XX
KW   Electron-transfer group; ETM; mismatch; genotyping;
KW   gene expression; ss.
XX
OS   Synthetic.
XX
PN   WO200107665-A2.
XX
PD   01-FEB-2001.
XX
PF   26-JUL-2000; 2000WO-US20476.
XX
PR   26-JUL-1999;   99US-0145695.
PR   17-MAR-2000; 2000US-0190259.
XX
```

PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI; 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface -
XX
PS Example 6; Page 128; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

Query Match 11.3%; Score 81; DB 22; Length 936;
Best Local Similarity 1.0%; Pred. No. 1.2e-13;
Matches 6; Conservative 362; Mismatches 237; Indels 0; Gaps 0;

```
Qy    110 ttaatgtcaaggtcattctagaagagctcatagtgagaggccatgaggtaacagtattga 169
          ::::: : ::  : ::: :: :: :  : ::: : : :    :: :  ::: : :::: :
Db    664 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 605

Qy    170 ctcactcaaagccttcgttaattgactacaggaagccttctgcattgaaatttgaggtgg 229
           : : : :::  |::  :::::: : :: :  ::   :: :  ::: :::::: : :
Db    604 WWWWWWWWWWWWCWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 545

Qy    230 tccatatgccacaggacagaacagaagaaaatgaaatatttgttgacctagctctgaatg 289
          :  ::::   : :  : : :: : :: ::::: :::::::: ::.:  ::| : : :::
Db    544 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWGWWWWWWWWW 485

Qy    290 tcttgccaggcttatcaacctggcaatcagttataaaattaaatgatttttttgttgaaa 349
          : ::   :   :::: ::  :   ::: : :::::::::::::: :::::::: :: :::
Db    484 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 425

Qy    350 taagaggaactttaaaaatgatgtgtgagagctttatctacaatcagacacttatgaaga 409
          ::: :  :: :::::::::: :: : : : |   :::: :: ::: : : : :::: :: :
Db    424 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWTAAGCWWWWWWWWWWWWWWWWWWWWWWWWW 365

Qy    410 agctacaggaaaccaactacgatgtaacgcttatagaccctgtgattccccgtggagacc 469
          :  :: :  :::  :: ::  :: :::   ::::: :  : : :::     :  : :
Db    364 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 305

Qy    470 tgatggctgagttgcttccagtccctttgtgctcacacttagaacttctctaagaggca 529
          : ::   : :|::  ::  : :   :::: :  : : : ::: :: :: : ::: :   :
Db    304 WWWWWWWWWWGWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 245

Qy    530 atatggagcgaagctgtgggaaacttccagctccactttcctatgtacctgtgcctatga 589
          :::: :   ::  : :   ::: ::  :  :  : ::: ::: :: |: :   ::: :
Db    244 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWCWWWWWWWWW 185

Qy    590 caggactaacagacagaatgacctttctggaaagagtaaaaaattcaatgctttcagttt 649
           :  : ::: : : : ::: :  ::: :  ::: : :::::::: :::  ::: : :::
Db    184 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 125

Qy    650 tgttccacttctggattcaggattacgactatcatttttgggaagagttttatagtaagg 709
          : ::  : :: :  ::: :  :::: |: ::: :::::   :: : :::::::: :::
Db    124 WWWWWWWWWWWWWWWWWWWWWWWWWWWWGWWWWWWWWWWWWWWWWWWWWWWWWWWWW 65

Qy    710 catta 714
            ::::
Db     64 WWWWW 60
```

Search completed: August 27, 2001, 18:00:29

Job time: 8372 sec